

#6
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Page 1 of 7

1643

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/503,089A

DATE: 08/09/2000
TIME: 15:22:36

Input Set : A:\09503089.app
Output Set: N:\CRF3\08092000\I503089A.raw

ENTERED

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3 <110> APPLICANT: PATEL, AMANDA J.
4 HONORE, ERIC
5 LESAGE, FLORIAN
6 ROMÉY, GEORGES
7 LAZDUSKI, MICHEL
9 <120> TITLE OF INVENTION: A method for the identification of anesthetics
11 <130> FILE REFERENCE: f17b12prov3-humanTREK
13 <140> CURRENT APPLICATION NUMBER: 09/503,089A
14 <141> CURRENT FILING DATE: 2000-02-11
16 <160> NUMBER OF SEQ ID NOS: 5
18 <170> SOFTWARE: Microsoft Word 2000
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21 <211> LENGTH: 1236
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1236)
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32 1 5 10 15
34 aaa ccg agg ctc tcg ttt tcc acg aaa ccc aca gtg ctt gct tcc cgg 96
35 Lys Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg
36 20 25 30
38 gtg gag agt gac acg acc att aat gtt atg aaa tgg aag acg gtc tcc 144
39 Val Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser
40 35 40 45
42 acg ata ttc ctg gtg gtt gtc ctc tat ctg atc atc gga gcc acc gtg 192
43 Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val
44 50 55 60
46 ttc aaa gca ttg gag cag cct cat gag att tca cag agg acc acc att 240
47 Phe Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile
48 65 70 75 80
50 gtg atc cag aag caa aca ttc ata tcc caa cat tcc tgt gtc aat tcg 288
51 Val Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser
52 85 90 95
54 acg gag ctg gat gaa ctc att cag caa ata gtg gca gca ata aat gca 336
55 Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala
56 100 105 110
58 ggg att ata ccg tta gga aac acc tcc aat caa atc agt cac tgg gat 384
59 Gly Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp
60 115 120 125
62 ttg gga agt tcc ttc ttc ttt gct ggc act gtt att aca acc ata gga 432
63 Leu Gly Ser Ser Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly
64 130 135 140
65 ttt gga aac atc tca cca cgc aca gaa ggc ggc aaa ata ttc tgt atc 480
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66 Phe Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile
67 145 150 155 160
69 atc tat gcc tta ctg gga att ccc ctc ttt ggt ttt ctc ttg gct gga 528
70 Ile Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly
71 165 170 175
73 gtt gga gat cag cta ggc acc ata ttt gga aaa gga att gcc aaa gtg 576
74 Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val
75 180 185 190
77 gaa gat acg ttt att aag tgg aat gtt agt cag acc aag att cgc atc 624
78 Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile
79 195 200 205
81 atc tca aca atc ata ttt ata cta ttt ggc tgt gta ctc ttt gtg gct 672
82 Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala
83 210 215 220
85 ctg cct gcg atc ata ttc aaa cac ata gaa ggc tgg agt gcc ctg gac 720
86 Leu Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp
87 225 230 235 240
89 gcc att tat ttt gtg gtt atc act cta aca act att gga ttt ggt gac 768
90 Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp
91 245 250 255
93 tac gtt gca ggt gga tcc gat att gaa tat ctg gac ttc tat aag cct 816
94 Tyr Val Ala Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro
95 260 265 270
97 gtc gtg tgg ttc tgg atc ctt gta ggg ctt gct tac ttt gct gct gtc 864
98 Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val
99 275 280 285
101 ctg agc atg att gga gat tgg ctc cga gtg ata tct aaa aag aca aaa 912
102 Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys
103 290 295 300
105 gaa gag gtg gga gag ttc aga gca cac gct gct gag tgg aca gcc aac 960
106 Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn
107 305 310 315 320
109 gtc aca gcc gaa ttc aaa gaa acc agg agg cga ctg agt gtg gag att 1008
110 Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile
111 325 330 335
113 tat gac aag ttc cag cgg gcc acc tcc atc aag cgg aag ctc tcg gca 1056
114 Tyr Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala
115 340 345 350
117 gaa ctg gct gga aac cac aat cag gag ctg act cct tgt agg agg acc 1104
118 Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr
119 355 360 365
121 ctg tca gtg aac cac ctg acc aac gag agg gat gtc ttg cct ccc tta 1152
122 Leu Ser Val Asn His Leu Thr Asn Glu Arg Asp Val Leu Pro Pro Leu
123 370 375 380
125 ctg aag act gag agt atc tat ctg aat ggt ttg acg cca cac tgt gct 1200
126 Leu Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Thr Pro His Cys Ala
127 385 390 395 400
129 ggt gaa gag att gct gtg att gag aac atc aaa tag 1236
130 Gly Glu Glu Ile Ala Val Ile Glu Asn Ile Lys

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131                               405                               410
134 <210> SEQ ID NO: 2
135 <211> LENGTH: 411
136 <212> TYPE: PRT ✓
137 <213> ORGANISM: Homo sapiens ✓
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143   20                               25                               30
144 Val Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser
145   35                               40                               45
146 Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val
147   50                               55                               60
148 Phe Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile
149   65                               70                               75                               80
150 Val Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser
151   85                               90                               95
152 Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala
153   100                              105                              110
154 Gly Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp
155   115                              120                              125
156 Leu Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly
157   130                              135                              140
158 Phe Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile
159   145                              150                              155                              160
160 Ile Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly
161   165                              170                              175
162 Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val
163   180                              185                              190
164 Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile
165   195                              200                              205
166 Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala
167   210                              215                              220
168 Leu Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp
169   225                              230                              235                              240
170 Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp
171   245                              250                              255
172 Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro
173   260                              265                              270
174 Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val
175   275                              280                              285
176 Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys
177   290                              295                              300
178 Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn
179   305                              310                              315                              320
180 Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Leu Ser Val Glu Ile
181   325                              330                              335
182 Tyr Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala

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183          340          345          350
184 Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr
185          355          360          365
186 Leu Ser Val Asn His Leu Thr Asn Glu Arg Asp Val Leu Pro Pro Leu
187          370          375          380
188 Leu Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Thr Pro His Cys Ala
189 385          390          395          400
190 Gly Glu Glu Ile Ala Val Ile Glu Asn Ile Lys
191          405          410
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195 <211> LENGTH: 3580
196 <212> TYPE: DNA
197 <213> ORGANISM: Mus musculus
199 <220> FEATURE:
200 <221> NAME/KEY: CDS
201 <222> LOCATION: (484)..(1719)
203 <400> SEQUENCE: 3
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208 gaagaggggc tgcagtgate accccctcgc tgagccccgg ggcagagccc agccgcccgc 180
210 cgagcgacac gagccacggg ccgagcgcac ccaggggccc cgcgggaccc caggcgccca 240
212 cgcaatcggg gtgaccatc gcgcgcgggg gcgtcgtcgt ccgatcccaa cttggcctcg 300
214 gcctcgcctt ctgccacgcc tgcacccgct ggtgtcctct ccttcggcg atttcgtttc 360
216 ttctcacgct cccctctcta taccctccc gcctccagcc ccgctctccc cacottgtaa 420
218 aacaaagccg gggaaaaatgc ctaccgtgc agctcggagc gcgcagcccg tcttgggaata 480
220 agg`atg gcg gcc cct gac ttg ctg gat ccc aag tct gct gct cag aac 528
221 Met Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn
222 1 5 10 15
224 tcc aaa ccg agg ctc tca ttc tcc tca aaa ccc acc gtg ctt gct tcc 576
225 Ser Lys Pro Arg Leu Ser Phe Ser Ser Lys Pro Thr Val Leu Ala Ser
226 20 25 30
228 cgg gtg gag agt gac tcg gcc att aat gtt atg aaa tgg aag aca gtc 624
229 Arg Val Glu Ser Asp Ser Ala Ile Asn Val Met Lys Trp Lys Thr Val
230 35 40 45
232 tcc acg att ttc ctg gtg gtc gtc ctc tac ctg atc atc gga gcc gcg 672
233 Ser Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Ala
234 50 55 60
236 gtg ttc aag gca ttg gag cag cct cag gag att tcc cag agg acc acc 720
237 Val Phe Lys Ala Leu Glu Gln Pro Gln Glu Ile Ser Gln Arg Thr Thr
238 65 70 75
240 att gtg atc cag aag cag acc ttc ata gcc cag cat gcc tgc gtc aac 768
241 Ile Val Ile Gln Lys Gln Thr Phe Ile Ala Gln His Ala Cys Val Asn
242 80 85 90 95
244 tcc acc gag ctg gac gaa ctc atc cag caa ata gtg gca gca ata aac 816
245 Ser Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn
246 100 105 110
248 gca ggg att atc ccc tta gga aac agc tcc aat caa gtt agt cac tgg 864
249 Ala Gly Ile Ile Pro Leu Gly Asn Ser Ser Asn Gln Val Ser His Trp
250 115 120 125

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252	gac	ctc	gga	agc	tct	ttc	ttc	ttt	gct	ggt	act	gtt	atc	aca	acc	ata	912
253	Asp	Leu	Gly	Ser	Ser	Phe	Phe	Phe	Ala	Gly	Thr	Val	Ile	Thr	Thr	Ile	
254			130					135					140				
256	gga	ttt	gga	aac	atc	tcc	cca	cga	act	gaa	ggt	gga	aaa	ata	ttc	tgc	960
257	Gly	Phe	Gly	Asn	Ile	Ser	Pro	Arg	Thr	Glu	Gly	Gly	Lys	Ile	Phe	Cys	
258		145					150					155					
260	atc	atc	tat	gcc	ttg	ctg	gga	att	ccc	ctc	ttt	ggc	ttt	cta	ctg	gct	1008
261	Ile	Ile	Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Phe	Gly	Phe	Leu	Leu	Ala	
262	160					165				170						175	
264	ggg	gtt	ggt	gat	cag	cta	gga	act	ata	ttt	gga	aaa	gga	att	gcc	aaa	1056
265	Gly	Val	Gly	Asp	Gln	Leu	Gly	Thr	Ile	Phe	Gly	Lys	Gly	Ile	Ala	Lys	
266				180						185					190		
268	gtg	gaa	gac	aca	ttt	att	aag	tgg	aat	gtt	agt	cag	acg	aag	att	cgt	1104
269	Val	Glu	Asp	Thr	Phe	Ile	Lys	Trp	Asn	Val	Ser	Gln	Thr	Lys	Ile	Arg	
270				195					200					205			
272	atc	atc	tcc	acc	atc	atc	ttc	atc	ctg	ttt	ggc	tgt	gtc	ctc	ttt	gtg	1152
273	Ile	Ile	Ser	Thr	Ile	Ile	Phe	Ile	Leu	Phe	Gly	Cys	Val	Leu	Phe	Val	
274			210				215						220				
276	gct	ctc	cct	gcg	gtc	ata	ttc	aag	cac	ata	gaa	ggc	tgg	agc	gcc	ctg	1200
277	Ala	Leu	Pro	Ala	Val	Ile	Phe	Lys	His	Ile	Glu	Gly	Trp	Ser	Ala	Leu	
278		225				230						235					
280	gac	gct	atc	tat	ttt	gtg	gtt	atc	act	ctg	acg	acc	att	gga	ttt	gga	1248
281	Asp	Ala	Ile	Tyr	Phe	Val	Val	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	
282	240					245					250				255		
284	gac	tac	gtg	gca	ggt	gga	tca	gac	att	gaa	tat	ctg	gac	ttc	tac	aag	1296
285	Asp	Tyr	Val	Ala	Gly	Gly	Ser	Asp	Ile	Glu	Tyr	Leu	Asp	Phe	Tyr	Lys	
286				260						265				270			
288	cct	gtg	gtg	tgg	ttc	tgg	atc	ctc	gtt	ggg	ctg	gcc	tac	ttt	gca	gct	1344
289	Pro	Val	Val	Trp	Phe	Trp	Ile	Leu	Val	Gly	Leu	Ala	Tyr	Phe	Ala	Ala	
290			275						280					285			
292	gtt	ctg	agc	atg	att	ggg	gac	tgg	cta	cgg	gtg	atc	tct	aag	aag	acg	1392
293	Val	Leu	Ser	Met	Ile	Gly	Asp	Trp	Leu	Arg	Val	Ile	Ser	Lys	Lys	Thr	
294			290				295						300				
296	aag	gaa	gag	gtg	gga	gag	ttc	aga	gcg	cat	gcc	gct	gag	tgg	aca	gcc	1440
297	Lys	Glu	Glu	Val	Gly	Glu	Phe	Arg	Ala	His	Ala	Ala	Glu	Trp	Thr	Ala	
298		305				310						315					
300	aat	gtc	acg	gcc	gag	ttc	aag	gaa	acg	agg	agg	cgg	ctg	agc	gtg	gag	1488
301	Asn	Val	Thr	Ala	Glu	Phe	Lys	Glu	Thr	Arg	Arg	Arg	Leu	Ser	Val	Glu	
302	320					325					330				335		
304	atc	tac	gac	aag	ttc	cag	cgt	gcc	aca	tcc	gtg	aag	cgg	aag	ctc	tcc	1536
305	Ile	Tyr	Asp	Lys	Phe	Gln	Arg	Ala	Thr	Ser	Val	Lys	Arg	Lys	Leu	Ser	
306				340						345				350			
308	gca	gag	ctg	gcg	ggc	aac	cac	aac	cag	gaa	ctg	act	ccg	tgt	agg	agg	1584
309	Ala	Glu	Leu	Ala	Gly	Asn	His	Asn	Gln	Glu	Leu	Thr	Pro	Cys	Arg	Arg	
310			355						360					365			
312	acc	ctg	tct	gtg	aac	cac	ctg	acc	agc	gag	agg	gaa	gtc	ctg	cct	ccc	1632
313	Thr	Leu	Ser	Val	Asn	His	Leu	Thr	Ser	Glu	Arg	Glu	Val	Leu	Pro	Pro	
314			370				375						380				
316	ttg	ctg	aag	gct	gag	agc	atc	tat	ctg	aac	ggt	ctg	aca	cca	cac	tgt	1680

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